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## RAW SEQUENCE LISTING

DATE: 02/06/2002

PATENT APPLICATION: US/09/900,379

TIME: 09:51:06

Input Set : N:\Crf3\RULE60\09900379.raw

Output Set: N:\CRF3\02062002\I900379.raw

## SEQUENCE LISTING

ENTERED

## 3 (1) GENERAL INFORMATION:

(i) APPLICANT: Wong, Hing C.  
 Rhode, Peter R.  
 Widanz, Jon A.  
 Grammer, Susan  
 Edwards, Ana C.  
 Chavaillaz, Pierre-Andre  
 Jiao, Jin-An

13 (ii) TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF

15 (iii) NUMBER OF SEQUENCES: 123

17 (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Dade International, Inc.  
 (B) STREET: 1717 Deerfield Road  
 (C) CITY: Deerfield  
 (D) STATE: Illinois  
 (E) COUNTRY: USA  
 (F) ZIP: 60015

25 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
 (B) COMPUTER: IBM PC compatible  
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

31 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/09/900,379  
 (B) FILING DATE: 06-Jul-2001  
 (C) CLASSIFICATION:

47 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US/08/776,084  
 (B) FILING DATE:  
 (A) APPLICATION NUMBER: PCT/US95/09816  
 (B) FILING DATE: 31-JUL-1995  
 (A) APPLICATION NUMBER: US 08/382,454  
 (B) FILING DATE: 01-FEB-1995  
 (A) APPLICATION NUMBER: US 08/283,302  
 (B) FILING DATE: 29-JUL-1994

51 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Pearson, Louise S.  
 (B) REGISTRATION NUMBER: 32,369  
 (C) REFERENCE/DOCKET NUMBER: STR-4665-CIP2

56 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (708) 267-5300  
 (B) TELEFAX: (708) 267-5376

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Input Set : N:\Crf3\RULE60\09900379.raw

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## 61 (2) INFORMATION FOR SEQ ID NO: 1:

## 63 (i) SEQUENCE CHARACTERISTICS:

64 (A) LENGTH: 10 amino acids

65 (B) TYPE: amino acid

66 (C) STRANDEDNESS: unknown

67 (D) TOPOLOGY: unknown

## 69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

71 Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly

72 1 5 10

## 74 (2) INFORMATION FOR SEQ ID NO: 2:

## 76 (i) SEQUENCE CHARACTERISTICS:

77 (A) LENGTH: 8 base pairs

78 (B) TYPE: nucleic acid

79 (C) STRANDEDNESS: unknown

80 (D) TOPOLOGY: unknown

## 82 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

84 CCACCATG

8

## 87 (2) INFORMATION FOR SEQ ID NO: 3:

## 89 (i) SEQUENCE CHARACTERISTICS:

90 (A) LENGTH: 18 amino acids

91 (B) TYPE: amino acid

92 (C) STRANDEDNESS: unknown

93 (D) TOPOLOGY: unknown

## 95 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

97 Ser Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala

98 1 5 10 15

100 Gly Arg

## 103 (2) INFORMATION FOR SEQ ID NO: 4:

## 105 (i) SEQUENCE CHARACTERISTICS:

106 (A) LENGTH: 18 amino acids

107 (B) TYPE: amino acid

108 (C) STRANDEDNESS: unknown

109 (D) TOPOLOGY: unknown

## 111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

114 Ser Ile Ser Gln Ala Val His Ala Ala Arg Ala Glu Ile Asn Glu Ala

115 1 5 10 15

117 Gly Arg

## 120 (2) INFORMATION FOR SEQ ID NO: 5:

## 122 (i) SEQUENCE CHARACTERISTICS:

123 (A) LENGTH: 18 amino acids

124 (B) TYPE: amino acid

125 (C) STRANDEDNESS: unknown

126 (D) TOPOLOGY: unknown

## 128 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

130 Ser Ile Ser Gln Ala Val His Ala Ala His Tyr Glu Ile Asn Glu Ala

131 1 5 10 15

133 Gly Arg

## 136 (2) INFORMATION FOR SEQ ID NO: 6:

## 138 (i) SEQUENCE CHARACTERISTICS:

## RAW SEQUENCE LISTING

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Input Set : N:\Crf3\RULE60\09900379.raw

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140      (A) LENGTH: 13 amino acids
141      (B) TYPE: amino acid
142      (C) STRANDEDNESS: unknown
143      (D) TOPOLOGY: unknown
145      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
147      Asn Leu Cys Asn Ile Pro Cys Ser Ala Leu Leu Ser Ser
148      1          5          10
151 (2) INFORMATION FOR SEQ ID NO: 7:
153      (i) SEQUENCE CHARACTERISTICS:
154          (A) LENGTH: 11 amino acids
155          (B) TYPE: amino acid
156          (C) STRANDEDNESS: unknown
157          (D) TOPOLOGY: unknown
159      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
161      Gln Ile Ser Val Gln Pro Ala Phe Ser Val Gln
162      1          5          10
165 (2) INFORMATION FOR SEQ ID NO: 8:
167      (i) SEQUENCE CHARACTERISTICS:
168          (A) LENGTH: 13 amino acids
169          (B) TYPE: amino acid
170          (C) STRANDEDNESS: unknown
171          (D) TOPOLOGY: unknown
173      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
175      Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
176      1          5          10
179 (2) INFORMATION FOR SEQ ID NO: 9:
181      (i) SEQUENCE CHARACTERISTICS:
182          (A) LENGTH: 13 amino acids
183          (B) TYPE: amino acid
184          (C) STRANDEDNESS: unknown
185          (D) TOPOLOGY: unknown
187      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
189      His Tyr Gly Ser Leu Pro Gln Lys Ser Gln His Gly Arg
190      1          5          10
193 (2) INFORMATION FOR SEQ ID NO: 10:
195      (i) SEQUENCE CHARACTERISTICS:
196          (A) LENGTH: 13 amino acids
197          (B) TYPE: amino acid
198          (C) STRANDEDNESS: unknown
199          (D) TOPOLOGY: unknown
201      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
203      His Ser Leu Gly Lys Trp Leu Gly His Pro Asp Lys Phe
204      1          5          10
207 (2) INFORMATION FOR SEQ ID NO: 11:
209      (i) SEQUENCE CHARACTERISTICS:
210          (A) LENGTH: 14 amino acids
211          (B) TYPE: amino acid
212          (C) STRANDEDNESS: unknown
213          (D) TOPOLOGY: unknown

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215 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
 217 Met Ala Ser Gln Lys Arg Pro Ser Gln Arg Ser Lys Tyr Leu  
 218 1 5 10

221 (2) INFORMATION FOR SEQ ID NO: 12:  
 223 (i) SEQUENCE CHARACTERISTICS:  
 224 (A) LENGTH: 27 base pairs  
 225 (B) TYPE: nucleic acid  
 226 (C) STRANDEDNESS: unknown  
 227 (D) TOPOLOGY: unknown

229 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
 231 GCAGAAGAAT TCGAGCTCGG CCCCCAG 27

234 (2) INFORMATION FOR SEQ ID NO: 13:  
 236 (i) SEQUENCE CHARACTERISTICS:  
 237 (A) LENGTH: 33 base pairs  
 238 (B) TYPE: nucleic acid  
 239 (C) STRANDEDNESS: unknown  
 240 (D) TOPOLOGY: unknown

242 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
 244 GATGATATCA GAGAGAAATA CATACTAACA CAC 33

247 (2) INFORMATION FOR SEQ ID NO: 14:  
 249 (i) SEQUENCE CHARACTERISTICS:  
 250 (A) LENGTH: 30 base pairs  
 251 (B) TYPE: nucleic acid  
 252 (C) STRANDEDNESS: unknown  
 253 (D) TOPOLOGY: unknown

255 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
 257 CGGAAGAAAG AGACTTCGGC CGCTACTTAC 30

260 (2) INFORMATION FOR SEQ ID NO: 15:  
 262 (i) SEQUENCE CHARACTERISTICS:  
 263 (A) LENGTH: 47 base pairs  
 264 (B) TYPE: nucleic acid  
 265 (C) STRANDEDNESS: unknown  
 266 (D) TOPOLOGY: unknown

268 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
 270 GTGTGTTAGT ATGTATTTCT CTCTGATATC TTCAGCTTCC AGCAGTG 47

273 (2) INFORMATION FOR SEQ ID NO: 16:  
 275 (i) SEQUENCE CHARACTERISTICS:  
 276 (A) LENGTH: 21 base pairs  
 277 (B) TYPE: nucleic acid  
 278 (C) STRANDEDNESS: unknown  
 279 (D) TOPOLOGY: unknown

281 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
 283 TCTTCTAGAA GACCACGCTA C 21

286 (2) INFORMATION FOR SEQ ID NO: 17:  
 288 (i) SEQUENCE CHARACTERISTICS:  
 289 (A) LENGTH: 36 base pairs  
 290 (B) TYPE: nucleic acid  
 291 (C) STRANDEDNESS: unknown  
 292 (D) TOPOLOGY: unknown

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Input Set : N:\Crf3\RULE60\09900379.raw

Output Set: N:\CRF3\02062002\I900379.raw

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294      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
296 GATGATATCC GGCCGAAGTC TCTTTCTTCC GTTGTC                      36
299 (2) INFORMATION FOR SEQ ID NO: 18:
301      (i) SEQUENCE CHARACTERISTICS:
302          (A) LENGTH: 24 base pairs
303          (B) TYPE: nucleic acid
304          (C) STRANDEDNESS: unknown
305          (D) TOPOLOGY: unknown
307      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
309 CAGGGTTATC AACACCCTGA AAAC                      24
311 (2) INFORMATION FOR SEQ ID NO: 19:
313      (i) SEQUENCE CHARACTERISTICS:
314          (A) LENGTH: 21 base pairs
315          (B) TYPE: nucleic acid
316          (C) STRANDEDNESS: unknown
317          (D) TOPOLOGY: unknown
319      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
321 GTCACAGTTA TCCACTCTGT C                          21
324 (2) INFORMATION FOR SEQ ID NO: 20:
326      (i) SEQUENCE CHARACTERISTICS:
327          (A) LENGTH: 38 base pairs
328          (B) TYPE: nucleic acid
329          (C) STRANDEDNESS: unknown
330          (D) TOPOLOGY: unknown
332      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:
334 CCGTCTCCTC AGGTACGGCC GGCCTCTCCA GGTCTTCG          38
339 (2) INFORMATION FOR SEQ ID NO: 21:
341      (i) SEQUENCE CHARACTERISTICS:
342          (A) LENGTH: 39 base pairs
343          (B) TYPE: nucleic acid
344          (C) STRANDEDNESS: unknown
345          (D) TOPOLOGY: unknown
347      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:
349 CACAGTTATC CACTCTGTCT TTGATATCAC AGGTGTCCT          39
352 (2) INFORMATION FOR SEQ ID NO: 22:
354      (i) SEQUENCE CHARACTERISTICS:
355          (A) LENGTH: 13 amino acids
356          (B) TYPE: amino acid
357          (C) STRANDEDNESS: unknown
358          (D) TOPOLOGY: unknown
360      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:
362      His Ser Leu Gly Lys Tyr Leu Gly His Pro Asp Lys Phe
363      1           5           10
366 (2) INFORMATION FOR SEQ ID NO: 23:
368      (i) SEQUENCE CHARACTERISTICS:
369          (A) LENGTH: 13 amino acids
370          (B) TYPE: amino acid
371          (C) STRANDEDNESS: unknown
372          (D) TOPOLOGY: unknown

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/900,379

DATE: 02/06/2002

TIME: 09:51:07

Input Set : N:\Crf3\RULE60\09900379.raw

Output Set: N:\CRF3\02062002\I900379.raw

L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:1888 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1892 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1896 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1900 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1904 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1908 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1912 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1916 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1920 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1925 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1929 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1933 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1937 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1941 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1945 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1949 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1953 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1957 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1961 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1965 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1969 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1973 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1977 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1981 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1985 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1990 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1994 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:1998 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:2002 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:2006 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:2010 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:2014 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122  
L:2035 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2039 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2043 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2047 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2051 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2056 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2060 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2064 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2068 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2072 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2076 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2080 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2084 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2088 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123

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Input Set : N:\Crf3\RULE60\09900379.raw

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L:2092 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2096 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2100 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
L:2104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123